

SEQUENCE LISTING

<110> IZUI, HIROSHI

MORIYA, MIKA

HIRANO, SEIKO

HARA, YOSHIHIKO

ITO, HISAO

MATSUI, KAZUHIKO

B1
<120> METHOD FOR PRODUCING L-GLUTAMIC ACID BY FERMENTATION ACCOMPANIED BY
PRECIPITATION

<130> 195942US0

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<170> PatentIn version 3.0

<210> 1

<211> 4556

<212> DNA

<213> Enterobacter agglomerans

<220>

<221> CDS

<222> (2) .. (121)

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<222> (322) .. (3129)

<220>

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Cys Pro Lys Gly Leu Asn Pro Thr Arg Ala Ile Gly His Ile Lys Ser	20	25	30	
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Met Leu Leu Gln Arg Ser Ala	35			
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			Met Gln	
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Asn Ser Ala Met Lys Pro Trp Leu Asp Ser Ser Trp Leu Ala Gly Ala	45	50	55	
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Asn Gln Ser Tyr Ile Glu Gln Leu Tyr Glu Asp Phe Leu Thr Asp Pro	60	65	70	
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Asp Ser Val Asp Ala Val Trp Arg Ser Met Phe Gln Gln Leu Pro Gly	75	80	85	
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Thr Gly Val Lys Pro Glu Gln Phe His Ser Ala Thr Arg Glu Tyr Phe	90	95	100	105
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Arg Arg Leu Ala Lys Asp Ala Ser Arg Tyr Thr Ser Ser Val Thr Asp	110	115	120	
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Pro Ala Thr Asn Ser Lys Gln Val Lys Val Leu Gln Leu Ile Asn Ala	125	130	135	
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Phe Arg Phe Arg Gly His Gln Glu Ala Asn Leu Asp Pro Leu Gly Leu	140	145	150	
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Trp Lys Gln Asp Arg Val Ala Asp Leu Asp Pro Ala Phe His Asp Leu	155	160	165	

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Phe	Thr	Ile	Thr	Asn	Gly	Gly	Val	Phe	Gly	Ser	Leu	Met	Ser	Thr										
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cca	atc	atc	aac	ccg	cca	cag	agc	gcg	att	ctg	ggc	atg	cac	gcc		4200								
Pro	Ile	Ile	Asn	Pro	Pro	Gln	Ser	Ala	Ile	Leu	Gly	Met	His	Ala										
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			1375					1380							

ggc	acg	cggtt	gcgtg	cccaa	tctca	atact	cttttc	cagat	ctgaat	ggat	agaac	atc			4436
-----	-----	-------	-------	-------	-------	-------	--------	-------	--------	------	-------	-----	--	--	------

atg	aac	tta	cac	gaa	tac	cag	gct	aaa	cag	ctg	ttt	gca	cgg	tat	4481
Met	Asn	Leu	His	Glu	Tyr	Gln	Ala	Lys	Gln	Leu	Phe	Ala	Arg	Tyr	
			1385					1390					1395		

ggc	atg	cca	gca	ccg	acc	ggc	tac	gcc	tgt	act	aca	cca	cgt	gaa	4526
Gly	Met	Pro	Ala	Pro	Thr	Gly	Tyr	Ala	Cys	Thr	Thr	Pro	Arg	Glu	
			1400					1405					1410		

gca	gaa	gaa	gcg	gca	tcg	aaa	atc	ggg	gca						4556
Ala	Glu	Glu	Ala	Ala	Ser	Lys	Ile	Gly	Ala						
			1415					1420							

<210> 2

<211> 39

<212> PRT

<213> Enterobacter agglomerans

<400> 2

Ala	Phe	Ser	Val	Phe	Arg	Cys	His	Ser	Ile	Met	Asn	Cys	Val	Ser	Val
1				5					10					15	

Cys	Pro	Lys	Gly	Leu	Asn	Pro	Thr	Arg	Ala	Ile	Gly	His	Ile	Lys	Ser
			20					25					30		

Met Leu Leu Gln Arg Ser Ala
35

<210> 3

<211> 935

<212> PRT

<213> Enterobacter agglomerans

<400> 3

Met Gln Asn Ser Ala Met Lys Pro Trp Leu Asp Ser Ser Trp Leu Ala
1 5 10 15

Gly Ala Asn Gln Ser Tyr Ile Glu Gln Leu Tyr Glu Asp Phe Leu Thr
20 25 30

Asp Pro Asp Ser Val Asp Ala Val Trp Arg Ser Met Phe Gln Gln Leu
35 40 45

Pro Gly Thr Gly Val Lys Pro Glu Gln Phe His Ser Ala Thr Arg Glu
50 55 60

Tyr Phe Arg Arg Leu Ala Lys Asp Ala Ser Arg Tyr Thr Ser Ser Val
65 70 75 80

Thr Asp Pro Ala Thr Asn Ser Lys Gln Val Lys Val Leu Gln Leu Ile
85 90 95

Asn Ala Phe Arg Phe Arg Gly His Gln Glu Ala Asn Leu Asp Pro Leu
100 105 110

Gly Leu Trp Lys Gln Asp Arg Val Ala Asp Leu Asp Pro Ala Phe His
115 120 125

Asp Leu Thr Asp Ala Asp Phe Gln Glu Ser Phe Asn Val Gly Ser Phe
130 135 140

Ala Ile Gly Lys Glu Thr Met Lys Leu Ala Asp Leu Phe Asp Ala Leu
145 150 155 160

Lys Gln Thr Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Ile Asn
165 170 175

Asn Thr Glu Glu Lys Arg Trp Ile Gln Gln Arg Ile Glu Ser Gly Ala
180 185 190

Ser Gln Thr Ser Phe Ser Gly Glu Glu Lys Lys Gly Phe Leu Lys Glu
195 200 205

Leu Thr Ala Ala Glu Gly Leu Glu Lys Tyr Leu Gly Ala Lys Phe Pro
210 215 220

Gly Ala Lys Arg Phe Ser Leu Glu Gly Gly Asp Ala Leu Val Pro Met
225 230 235 240

Leu Arg Glu Met Ile Arg His Ala Gly Lys Ser Gly Thr Arg Glu Val
245 250 255

Val Leu Gly Met Ala His Arg Gly Arg Leu Asn Val Leu Ile Asn Val
260 265 270

Leu Gly Lys Lys Pro Gln Asp Leu Phe Asp Glu Phe Ser Gly Lys His
275 280 285

Lys Glu His Leu Gly Thr Gly Asp Val Lys Tyr His Met Gly Phe Ser
290 295 300

Ser Asp Ile Glu Thr Glu Gly Gly Leu Val His Leu Ala Leu Ala Phe
305 310 315 320

Asn Pro Ser His Leu Glu Ile Val Ser Pro Val Val Met Gly Ser Val

325

330

335

Arg Ala Arg Leu Asp Arg Leu Ala Glu Pro Val Ser Asn Lys Val Leu
 340 345 350

Pro Ile Thr Ile His Gly Asp Ala Ala Val Ile Gly Gln Gly Val Val
 355 360 365

Gln Glu Thr Leu Asn Met Ser Gln Ala Arg Gly Tyr Glu Val Gly Gly
 370 375 380

Thr Val Arg Ile Val Ile Asn Asn Gln Val Gly Phe Thr Thr Ser Asn
 385 390 395 400

Pro Lys Asp Ala Arg Ser Thr Pro Tyr Cys Thr Asp Ile Gly Lys Met
 405 410 415

Val Leu Ala Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val
 420 425 430

Ala Phe Val Thr Arg Leu Ala Leu Asp Tyr Arg Asn Thr Phe Lys Arg
 435 440 445

Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu
 450 455 460

Ala Asp Glu Pro Ser Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys
 465 470 475 480

Lys His Pro Thr Pro Arg Lys Ile Tyr Ala Asp Arg Leu Glu Gly Glu
 485 490 495

Gly Val Ala Ser Gln Glu Asp Ala Thr Glu Met Val Asn Leu Tyr Arg
 500 505 510

Asp Ala Leu Asp Ala Gly Glu Cys Val Val Pro Glu Trp Arg Pro Met
 515 520 525

Ser Leu His Ser Phe Thr Trp Ser Pro Tyr Leu Asn His Glu Trp Asp
 530 535 540

Glu Pro Tyr Pro Ala Gln Val Asp Met Lys Arg Leu Lys Glu Leu Ala
 545 550 555 560

Leu Arg Ile Ser Gln Val Pro Glu Gln Ile Glu Val Gln Ser Arg Val
 565 570 575

Ala Lys Ile Tyr Asn Asp Arg Lys Leu Met Ala Glu Gly Glu Lys Ala
 580 585 590

Phe Asp Trp Gly Gly Ala Glu Asn Leu Ala Tyr Ala Thr Leu Val Asp
 595 600 605

Glu Gly Ile Pro Val Arg Leu Ser Gly Glu Asp Ser Gly Arg Gly Thr
 610 615 620

Phe Phe His Arg His Ala Val Val His Asn Gln Ala Asn Gly Ser Thr
 625 630 635 640

Tyr Thr Pro Leu His His Ile His Asn Ser Gln Gly Glu Phe Lys Val
 645 650 655

Trp Asp Ser Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly
 660 665 670

Tyr Ala Thr Ala Glu Pro Arg Val Leu Thr Ile Trp Glu Ala Gln Phe
 675 680 685

Gly Asp Phe Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser
 690 695 700

Ser Gly Glu Gln Lys Trp Gly Arg Met Cys Gly Leu Val Met Leu Leu
 705 710 715 720

Pro His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu
725 730 735

Glu Arg Tyr Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Cys Val
740 745 750

Pro Ser Thr Pro Ala Gln Val Tyr His Met Leu Arg Arg Gln Ala Leu
755 760 765

Arg Gly Met Arg Arg Pro Leu Val Val Met Ser Pro Lys Ser Leu Leu
770 775 780

Arg His Pro Leu Ala Ile Ser Ser Leu Asp Glu Leu Ala Asn Gly Ser
785 790 795 800

Phe Gln Pro Ala Ile Gly Glu Ile Asp Asp Leu Asp Pro Gln Gly Val
805 810 815

Lys Arg Val Val Leu Cys Ser Gly Lys Val Tyr Tyr Asp Leu Leu Glu
820 825 830

Gln Arg Arg Lys Asp Glu Lys Thr Asp Val Ala Ile Val Arg Ile Glu
835 840 845

Gln Leu Tyr Pro Phe Pro His Gln Ala Val Gln Glu Ala Leu Lys Ala
850 855 860

Tyr Ser His Val Gln Asp Phe Val Trp Cys Gln Glu Glu Pro Leu Asn
865 870 875 880

Gln Gly Ala Trp Tyr Cys Ser Gln His His Phe Arg Asp Val Val Pro
885 890 895

Phe Gly Ala Thr Leu Arg Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro
900 905 910

Ala Val Gly Tyr Met Ser Val His Gln Gln Gln Gln Gln Asp Leu Val

915

920

925

Asn Asp Ala Leu Asn Val Asn
 930 935

<210> 4

<211> 407

<212> PRT

<213> Enterobacter agglomerans

<400> 4

Met Ser Ser Val Asp Ile Leu Val Pro Asp Leu Pro Glu Ser Val Ala
 1 5 10 15

Asp Ala Thr Val Ala Thr Trp His Lys Lys Pro Gly Asp Ala Val Ser
 20 25 30

Arg Asp Glu Val Ile Val Glu Ile Glu Thr Asp Lys Val Val Leu Glu
 35 40 45

Val Pro Ala Ser Ala Asp Gly Val Leu Glu Ala Val Leu Glu Asp Glu
 50 55 60

Gly Ala Thr Val Thr Ser Arg Gln Ile Leu Gly Arg Leu Lys Glu Gly
 65 70 75 80

Asn Ser Ala Gly Lys Glu Ser Ser Ala Lys Ala Glu Ser Asn Asp Thr
 85 90 95

Thr Pro Ala Gln Arg Gln Thr Ala Ser Leu Glu Glu Glu Ser Ser Asp
 100 105 110

Ala Leu Ser Pro Ala Ile Arg Arg Leu Ile Ala Glu His Asn Leu Asp
 115 120 125

Ala Ala Gln Ile Lys Gly Thr Gly Val Gly Gly Arg Leu Thr Arg Glu
 130 135 140

Asp Val Glu Lys His Leu Ala Asn Lys Pro Gln Ala Glu Lys Ala Ala
 145 150 155 160

Ala Pro Ala Ala Gly Ala Ala Thr Ala Gln Gln Pro Val Ala Asn Arg
 165 170 175

Ser Glu Lys Arg Val Pro Met Thr Arg Leu Arg Lys Arg Val Ala Glu
 180 185 190

Arg Leu Leu Glu Ala Lys Asn Ser Thr Ala Met Leu Thr Thr Phe Asn
 195 200 205

Glu Ile Asn Met Lys Pro Ile Met Asp Leu Arg Lys Gln Tyr Gly Asp
 210 215 220

Ala Phe Glu Lys Arg His Gly Val Arg Leu Gly Phe Met Ser Phe Tyr
 225 230 235 240

Ile Lys Ala Val Val Glu Ala Leu Lys Arg Tyr Pro Glu Val Asn Ala
 245 250 255

Ser Ile Asp Gly Glu Asp Val Val Tyr His Asn Tyr Phe Asp Val Ser
 260 265 270

Ile Ala Val Ser Thr Pro Arg Gly Leu Val Thr Pro Val Leu Arg Asp
 275 280 285

Val Asp Ala Leu Ser Met Ala Asp Ile Glu Lys Lys Ile Lys Glu Leu
 290 295 300

Ala Val Lys Gly Arg Asp Gly Lys Leu Thr Val Asp Asp Leu Thr Gly
 305 310 315 320

Gly Asn Phe Thr Ile Thr Asn Gly Gly Val Phe Gly Ser Leu Met Ser
 325 330 335

Thr Pro Ile Ile Asn Pro Pro Gln Ser Ala Ile Leu Gly Met His Ala
 340 345 350

Ile Lys Asp Arg Pro Met Ala Val Asn Gly Gln Val Val Ile Leu Pro
 355 360 365

Met Met Tyr Leu Ala Leu Ser Tyr Asp His Arg Leu Ile Asp Gly Arg
 370 375 380

Glu Ser Val Gly Tyr Leu Val Ala Val Lys Glu Met Leu Glu Asp Pro
 385 390 395 400

Ala Arg Leu Leu Leu Asp Val
 405

<210> 5

<211> 40

<212> PRT

<213> Enterobacter agglomerans

<400> 5

Met Asn Leu His Glu Tyr Gln Ala Lys Gln Leu Phe Ala Arg Tyr Gly
 1 5 10 15

Met Pro Ala Pro Thr Gly Tyr Ala Cys Thr Thr Pro Arg Glu Ala Glu
 20 25 30

Glu Ala Ala Ser Lys Ile Gly Ala
 35 40

<210> 6

<211> 30

<212> DNA


<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Artificial Sequence: synthetic DNA


<400> 6

gtcgacaata gccygaatct gttctggtcg

30

<210> 7

<211> 30

<212> DNA

<213> Artibeus anderseni

<220>

<221> misc_feature

<222> ()..()

<223> Artificial Sequence: synthetic DNA

<400> 7

aagcttatcg acgctcccct ccccaccgtt

30

<210> 8
<211> 936
<212> PRT
<213> Escherichia coli

<400> 8

Met	Gln	Asn	Ser	Ala	Leu	Lys	Ala	Trp	Leu	Asp	Ser	Ser	Tyr	Leu	Ser
1				5					10					15	
Gly	Ala	Asn	Gln	Ser	Trp	Glu	Ile	Glu	Gln	Leu	Tyr	Glu	Asp	Phe	Leu
			20					25					30		
Thr	Asp	Pro	Asp	Ser	Val	Asp	Ala	Asn	Trp	Arg	Ser	Thr	Phe	Gln	Gln
		35					40					45			
Leu	Pro	Gly	Thr	Gly	Val	Lys	Pro	Asp	Gln	Phe	His	Ser	Gln	Thr	Arg
	50					55					60				
Glu	Tyr	Phe	Arg	Arg	Leu	Ala	Lys	Asp	Ala	Ser	Arg	Tyr	Ser	Ser	Thr
65					70					75					80
Ile	Ser	Asp	Pro	Asp	Thr	Asn	Val	Lys	Gln	Val	Lys	Val	Leu	Gln	Leu
				85					90					95	
Ile	Asn	Ala	Tyr	Arg	Phe	Arg	Gly	His	Gln	His	Ala	Asn	Leu	Asp	Pro
			100					105					110		
Leu	Gly	Leu	Trp	Gln	Gln	Asp	Lys	Val	Ala	Asp	Leu	Asp	Pro	Ser	Phe
		115					120					125			
His	Asp	Leu	Thr	Glu	Ala	Asp	Phe	Gln	Glu	Thr	Phe	Asn	Val	Gly	Ser
	130					135					140				
Phe	Ala	Ser	Gly	Lys	Glu	Thr	Met	Lys	Leu	Gly	Glu	Leu	Leu	Glu	Ala
145					150					155					160
Leu	Lys	Gln	Thr	Tyr	Cys	Gly	Pro	Ile	Gly	Ala	Glu	Tyr	Met	His	Ile
				165					170					175	
Thr	Ser	Thr	Glu	Glu	Lys	Arg	Trp	Ile	Gln	Gln	Arg	Ile	Glu	Ser	Gly
			180					185					190		
Arg	Ala	Thr	Phe	Asn	Ser	Glu	Glu	Lys	Lys	Arg	Phe	Leu	Ser	Glu	Leu

195

200

205

Thr	Ala	Ala	Glu	Gly	Leu	Glu	Arg	Tyr	Leu	Gly	Ala	Lys	Phe	Pro	Gly
210						215					220				
Ala	Lys	Arg	Phe	Ser	Leu	Glu	Gly	Gly	Asp	Ala	Leu	Ile	Pro	Met	Leu
225					230					235					240
Lys	Glu	Met	Ile	Arg	His	Ala	Gly	Asn	Ser	Gly	Thr	Arg	Glu	Val	Val
				245					250					255	
Leu	Gly	Met	Ala	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Asn	Val	Leu	Gly
			260					265					270		
Lys	Lys	Pro	Gln	Asp	Leu	Phe	Asp	Glu	Phe	Ala	Gly	Lys	His	Lys	Glu
		275					280					285			
His	Leu	Gly	Thr	Gly	Asp	Val	Lys	Tyr	His	Met	Gly	Phe	Ser	Ser	Asp
	290					295					300				
Phe	Gln	Thr	Asp	Gly	Gly	Leu	Val	His	Leu	Ala	Leu	Ala	Phe	Asn	Pro
305					310					315					320
Ser	His	Leu	Glu	Ile	Val	Ser	Pro	Val	Val	Ile	Gly	Ser	Val	Arg	Ala
				325					330					335	
Arg	Leu	Asp	Arg	Leu	Asp	Glu	Pro	Ser	Ser	Asn	Lys	Val	Leu	Pro	Ile
			340					345						350	
Thr	Ile	His	Gly	Asp	Ala	Ala	Val	Thr	Gly	Gln	Gly	Val	Val	Gln	Glu
		355					360					365			
Thr	Leu	Asn	Met	Ser	Lys	Ala	Arg	Gly	Tyr	Glu	Val	Gly	Gly	Thr	Val
	370					375					380				
Arg	Ile	Val	Ile	Asn	Asn	Gln	Val	Gly	Phe	Thr	Thr	Ser	Asn	Pro	Leu
385					390					395					400
Asp	Ala	Arg	Ser	Thr	Pro	Tyr	Cys	Thr	Asp	Ile	Gly	Lys	Met	Val	Gln
				405					410					415	
Ala	Pro	Ile	Phe	His	Val	Asn	Ala	Asp	Asp	Pro	Glu	Ala	Val	Ala	Phe
			420					425					430		
Val	Thr	Arg	Leu	Ala	Leu	Asp	Phe	Arg	Asn	Thr	Phe	Lys	Arg	Asp	Val
		435					440					445			
Phe	Ile	Asp	Leu	Val	Ser	Tyr	Arg	Arg	His	Gly	His	Asn	Asn	Glu	Ala
450						455					460				

Asp Glu Pro Ser Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys Lys
 465 470 475 480
 His Pro Thr Pro Arg Lys Ile Tyr Ala Asp Lys Leu Glu Gln Glu Lys
 485 490 495
 Val Ala Thr Leu Glu Asp Ala Thr Glu Met Val Asn Leu Tyr Arg Asp
 500 505 510
 Ala Leu Asp Ala Gly Asp Cys Val Val Ala Glu Trp Arg Pro Met Asn
 515 520 525
 Met His Ser Phe Thr Trp Ser Pro Tyr Leu Asn His Glu Trp Asp Glu
 530 535 540
 Glu Tyr Pro Asn Lys Val Glu Met Lys Arg Leu Gln Glu Leu Ala Lys
 545 550 555 560
 Arg Ile Ser Thr Val Pro Glu Ala Val Glu Met Gln Ser Arg Val Ala
 565 570 575
 Lys Ile Tyr Gly Asp Arg Gln Ala Met Ala Ala Gly Glu Lys Leu Phe
 580 585 590
 Asp Trp Gly Gly Ala Glu Asn Leu Ala Tyr Ala Thr Leu Val Asp Glu
 595 600 605
 Gly Ile Pro Val Arg Leu Ser Gly Glu Asp Ser Gly Arg Gly Thr Phe
 610 615 620
 Phe His Arg His Ala Val Ile His Asn Gln Ser Asn Gly Ser Thr Tyr
 625 630 635 640
 Thr Pro Leu Gln His Ile His Asn Gly Gln Gly Ala Phe Arg Val Trp
 645 650 655
 Asp Ser Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly Tyr
 660 665 670
 Ala Thr Ala Glu Pro Arg Thr Leu Thr Ile Trp Glu Ala Gln Phe Gly
 675 680 685
 Asp Phe Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser Ser
 690 695 700
 Gly Glu Gln Lys Trp Gly Arg Met Cys Gly Leu Val Met Leu Leu Pro
 705 710 715 720
 His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu Glu

725

730

735

Arg Tyr Leu Gln Leu Cys Ala Glu Gln Asn Asn Gln Val Cys Val Pro
 740 745 750
 Ser Thr Pro Ala Gln Val Tyr His Met Leu Arg Arg Gln Ala Leu Arg
 755 760 765
 Gly Met Arg Arg Pro Leu Val Val Met Ser Pro Lys Ser Leu Leu Arg
 770 775 780
 His Pro Leu Ala Val Ser Ser Leu Glu Glu Leu Ala Asn Gly Thr Phe
 785 790 795 800
 Leu Pro Ala Ile Gly Glu Glu Ile Asp Glu Leu Asp Pro Lys Gly Val
 805 810 815
 Lys Arg Val Val Met Cys Ser Ser Gly Lys Val Tyr Tyr Asp Leu Leu
 820 825 830
 Glu Gln Arg Arg Lys Asn Asn Gln His Asp Val Ala Ile Val Arg Ile
 835 840 845
 Glu Gln Leu Tyr Pro Phe Pro His Lys Ala Met Gln Glu Val Leu Gln
 850 855 860
 Gln Phe Ala His Val Lys Asp Phe Val Trp Cys Gln Glu Glu Pro Leu
 865 870 875 880
 Asn Gln Gly Ala Trp Tyr Cys Ser Gln His His Phe Arg Glu Val Ile
 885 890 895
 Pro Phe Gly Ala Ser Leu Arg Tyr Ala Gly Arg Pro Ala Ser Ala Ser
 900 905 910
 Pro Ala Val Gly Tyr Met Ser Val His Gln Lys Gln Gln Gln Asp Leu
 915 920 925
 Val Asn Asp Ala Leu Asn Val Glu
 930 935

<210> 9

<211> 405

<212> PRT

<213> Escherichia coli

<400> 9

Met	Ser	Ser	Val	Asp	Ile	Leu	Val	Pro	Asp	Leu	Pro	Glu	Ser	Val	Ala	
1				5					10					15		
Asp	Ala	Thr	Val	Ala	Thr	Trp	His	Lys	Lys	Pro	Gly	Asp	Ala	Val	Val	
			20					25					30			
Arg	Asp	Glu	Val	Leu	Val	Glu	Ile	Glu	Thr	Asp	Lys	Val	Val	Leu	Glu	
		35					40					45				
Val	Pro	Ala	Ser	Ala	Asp	Gly	Ile	Leu	Asp	Ala	Val	Leu	Glu	Asp	Glu	
	50					55					60					
Gly	Thr	Thr	Val	Thr	Ser	Arg	Gln	Ile	Leu	Gly	Arg	Leu	Arg	Glu	Gly	
65					70					75					80	
Asn	Ser	Ala	Gly	Lys	Glu	Thr	Ser	Ala	Lys	Ser	Glu	Glu	Lys	Ala	Ser	
				85					90					95		
Thr	Pro	Ala	Gln	Arg	Gln	Gln	Ala	Ser	Leu	Glu	Glu	Gln	Asn	Asn	Asp	
			100					105					110			
Ala	Leu	Ser	Pro	Ala	Ile	Arg	Arg	Leu	Leu	Ala	Glu	His	Asn	Leu	Asp	
		115					120					125				
Ala	Ser	Ala	Ile	Lys	Gly	Thr	Gly	Val	Gly	Gly	Arg	Leu	Thr	Arg	Glu	
	130					135					140					
Asp	Val	Glu	Lys	His	Leu	Ala	Lys	Ala	Pro	Ala	Lys	Glu	Ser	Ala	Pro	
145					150					155					160	
Ala	Ala	Ala	Ala	Pro	Ala	Ala	Gln	Pro	Ala	Leu	Ala	Ala	Arg	Ser	Glu	
				165					170					175		
Lys	Arg	Val	Pro	Met	Thr	Arg	Leu	Arg	Lys	Arg	Val	Ala	Glu	Arg	Leu	
			180					185					190			
Leu	Glu	Ala	Lys	Asn	Ser	Thr	Ala	Met	Leu	Thr	Thr	Phe	Asn	Glu	Val	
		195					200					205				
Asn	Met	Lys	Pro	Ile	Met	Asp	Leu	Arg	Lys	Gln	Tyr	Gly	Glu	Ala	Phe	
	210					215					220					
Glu	Lys	Arg	His	Gly	Ile	Arg	Leu	Gly	Phe	Met	Ser	Phe	Tyr	Val	Lys	
225					230					235					240	
Ala	Val	Val	Glu	Ala	Leu	Lys	Arg	Tyr	Pro	Glu	Val	Asn	Ala	Ser	Ile	

245

250

255

Asp Gly Asp Asp Val Val Tyr His Asn Tyr Phe Asp Val Ser Met Ala
 260 265 270

Val Ser Thr Pro Arg Gly Leu Val Thr Pro Val Leu Arg Asp Val Asp
 275 280 285

Thr Leu Gly Met Ala Asp Ile Glu Lys Lys Ile Lys Glu Leu Ala Val
 290 295 300

Lys Gly Arg Asp Gly Lys Leu Thr Val Glu Asp Leu Thr Gly Gly Asn
 305 310 315 320

Phe Thr Ile Thr Asn Gly Gly Val Phe Gly Ser Leu Met Ser Thr Pro
 325 330 335

Ile Ile Asn Pro Pro Gln Ser Ala Ile Leu Gly Met His Ala Ile Lys
 340 345 350

Asp Arg Pro Met Ala Val Asn Gly Gln Val Glu Ile Leu Pro Met Met
 355 360 365

Tyr Leu Ala Leu Ser Tyr Asp His Arg Leu Ile Asp Gly Arg Glu Ser
 370 375 380

Val Gly Phe Leu Val Thr Ile Lys Glu Leu Leu Glu Asp Pro Thr Arg
 385 390 395 400

Leu Leu Leu Asp Val
 405

<210> 10

<211> 41

<212> PRT

<213> Enterobacter agglomerans

<400> 10

Met Asn Leu His Glu Tyr Gln Ala Lys Gln Leu Phe Ala Arg Tyr Gly
 1 5 10 15

Met Pro Ala Pro Thr Gly Tyr Ala Cys Thr Thr Pro Arg Glu Ala Glu
 20 25 30

Glu Ala Ala Ser Lys Ile Gly Ala Gly
35 40

<210> 11

<211> 61

<212> PRT

<213> Escherichia coli

Bi
Eng
<400> 11

Met Asn Leu Glu His Glu Tyr Gln Ala Lys Gln Leu Phe Ala Arg Tyr
1 5 10 15

Gly Leu Pro Ala Pro Val Gly Tyr Ala Cys Tyr Tyr Pro Arg Glu Ala
20 25 30

Glu Glu Ala Ala Ser Lys Ile Gly Ala Gly Pro Trp Val Val Lys Cys
35 40 45

Gln Cys His Ala Gly Gly Arg Gly Lys Ala Gly Gly Val
50 55 60

<210> 12

<211> 58

<212> PRT

<213> Escherichia coli

<400> 12

Phe Leu Ile Asp Ser Arg Asp Thr Glu Thr Asp Ser Arg Leu Asp Gly
1 5 10 15

Leu Ser Asp Ala Phe Ser Val Phe Arg Cys His Ser Ile Met Asn Cys
20 25 30

Val Ser Cys Ser Pro Lys Gly Leu Asn Pro Thr Arg Ala Ile Gly His
35 40 45

Ile Lys Ser Met Leu Leu Gln Arg Asn Ala
50 55